

WGIN2 JIC Update

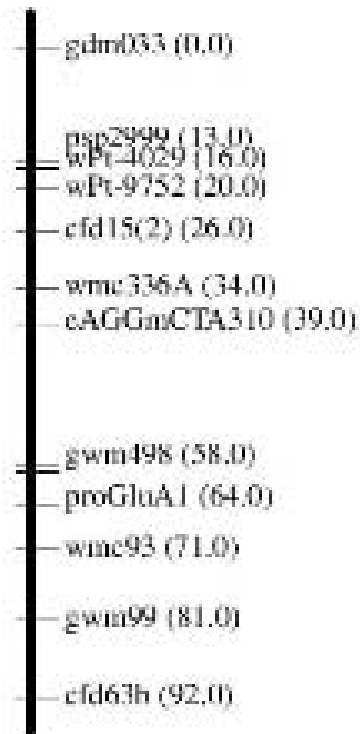
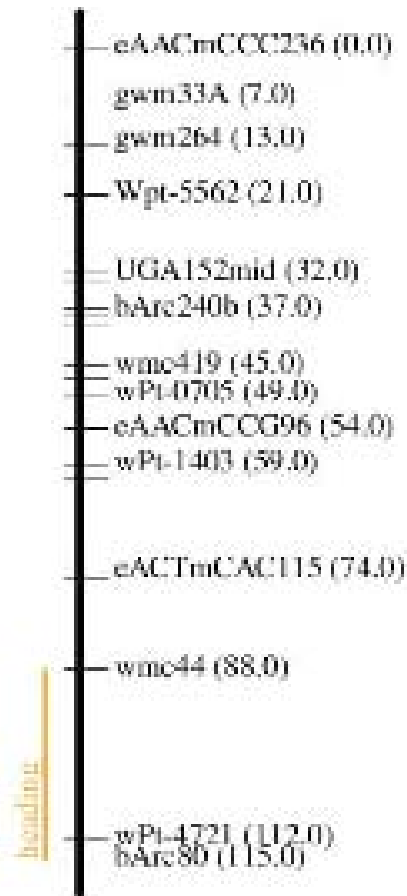
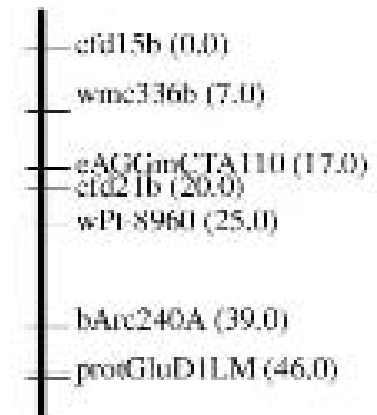
Management meeting Nov '10

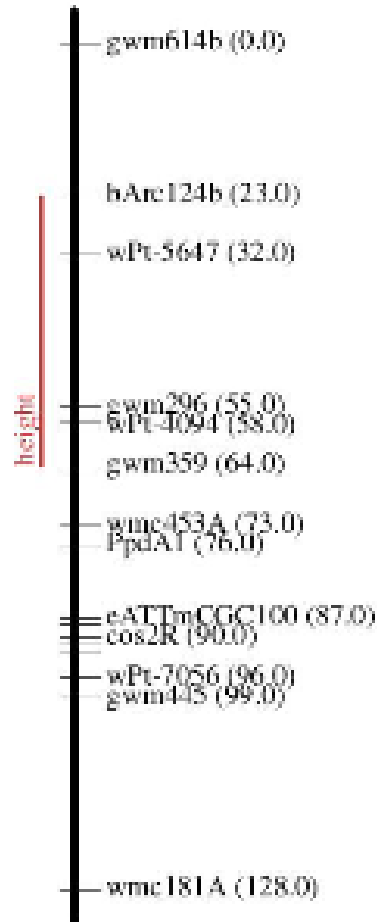
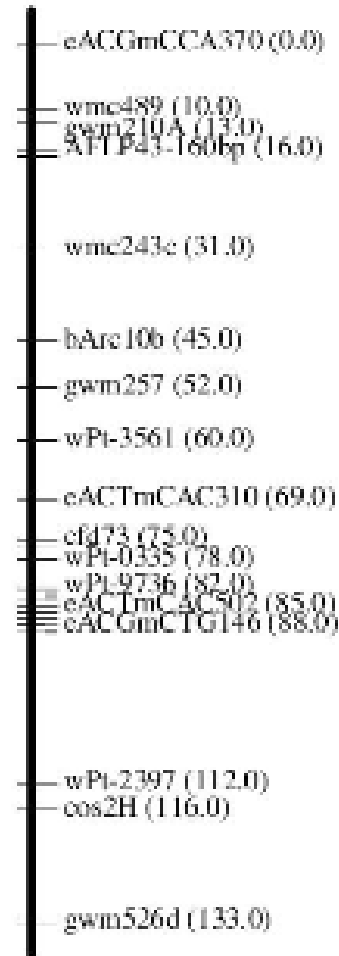
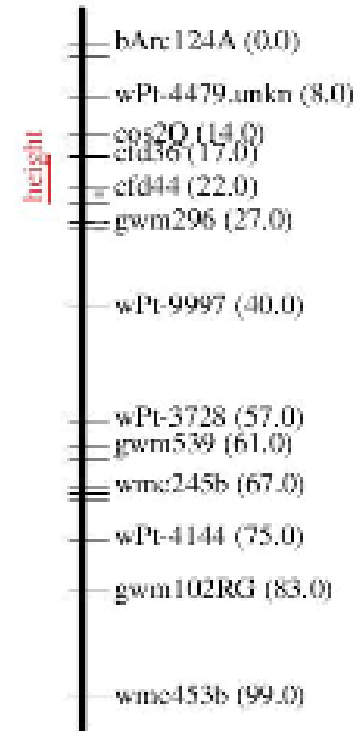
previous Aug '10

Development of Near Isogenic Lines

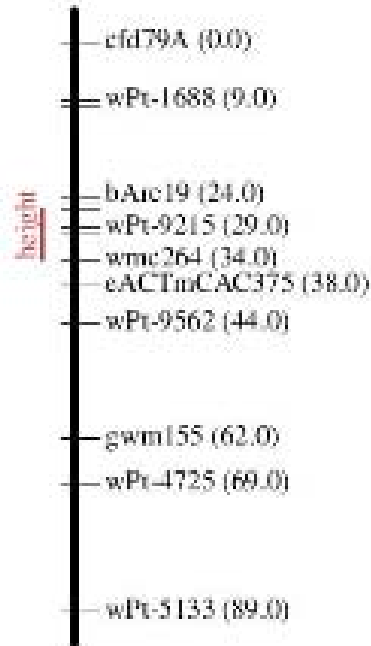
Avalon x Cadenza introgression segments- validation of allelic difference?
 Now selecting homozygotes from selfed BC₂ **Selected homozygotes out of vernalization**

1B	wmc44-barc80	
1D	gdm11-wmc93	
2A	barc124b-gwm122	
2D	gwm261-cfd36	
3A	wmc264-barc19	Some validation
3B	wm389-gwm493-barc75	
3B	cfd79b-wmc326	
6A	barc171-barc23a-gwm570	
6B	gwm219-wmc105	
7B	barc176-wmc517-gwm577	
7D	cfd21a-gwm437-ppsp3113	

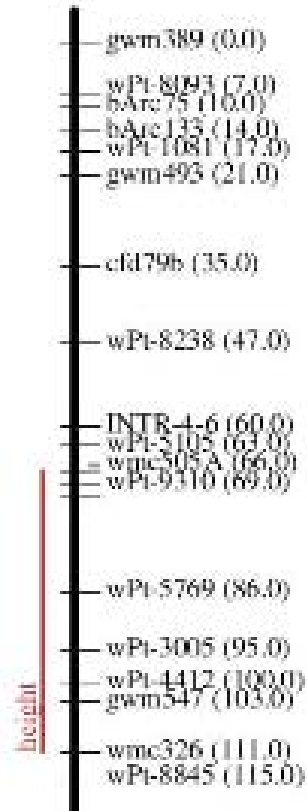
1A**1B****1D****1Dtelo**

2A**2B****2D****2Dtelo**

3A



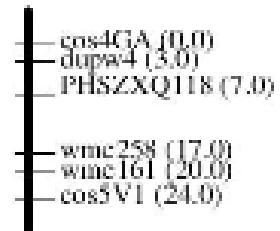
3B



3D



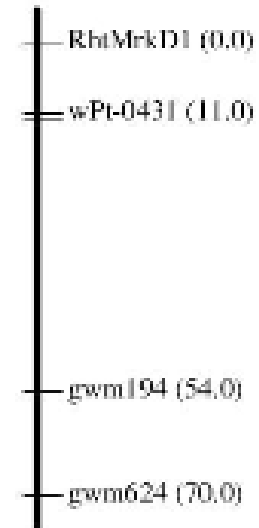
4A



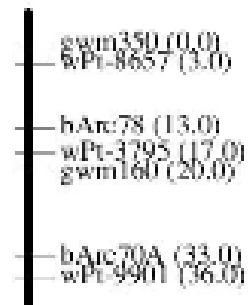
4B

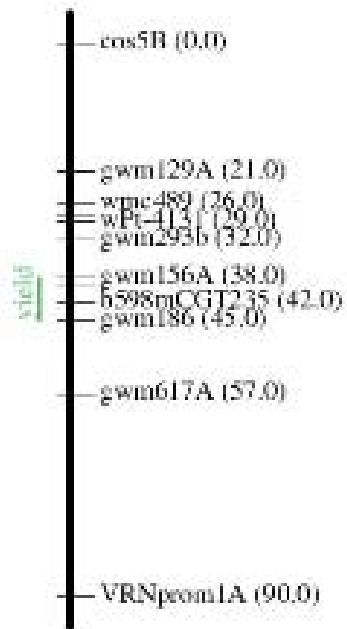
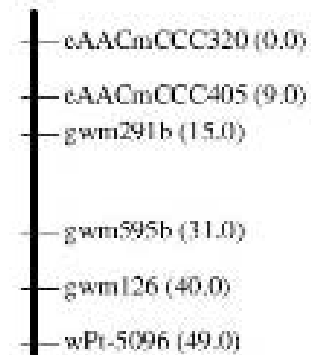
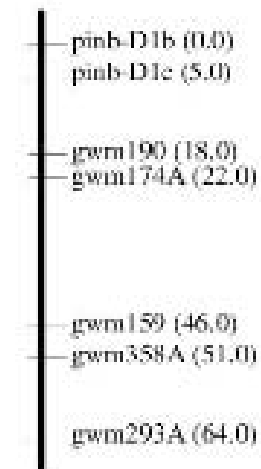


4D

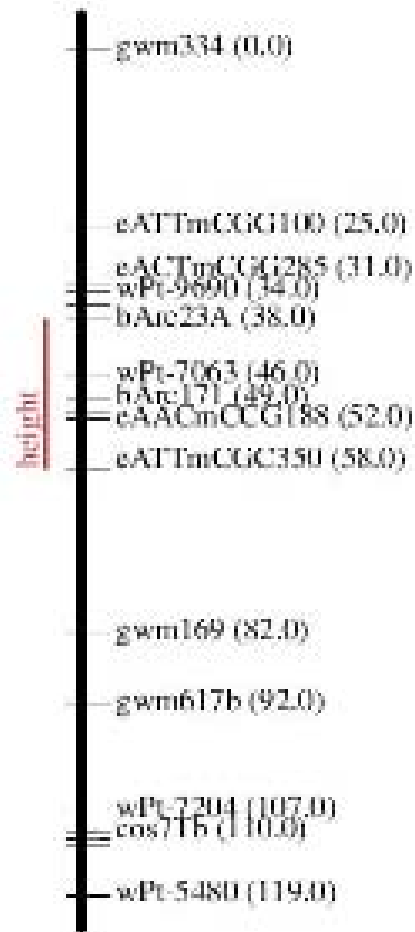


4Atelo

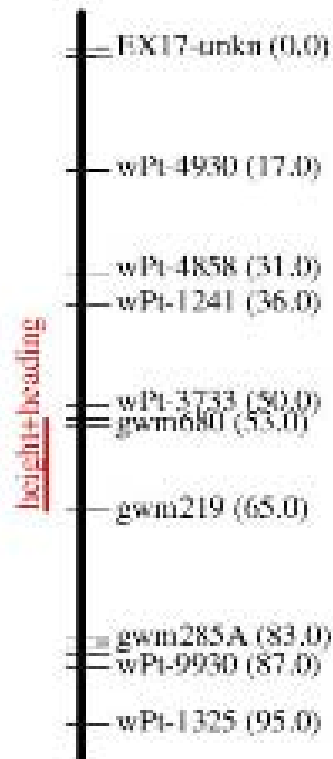


5A**5Atelo****5BL****5BS****5D****5Dtelo**

6A



6B



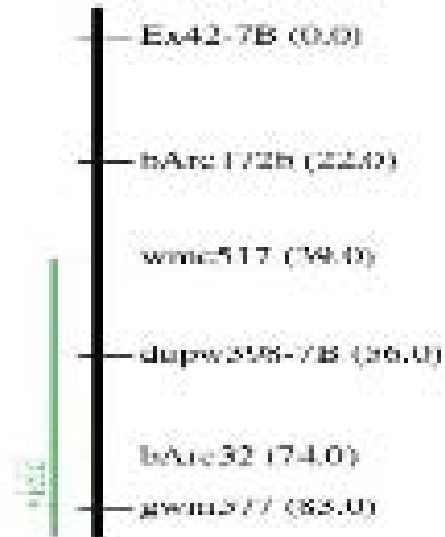
6D



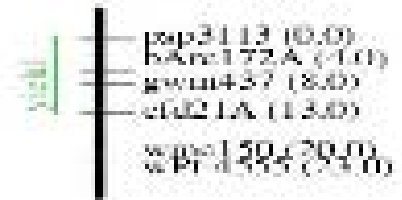
7A



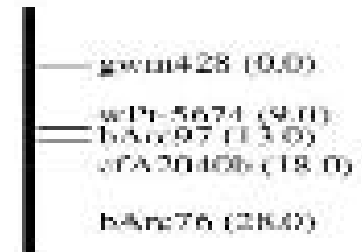
7BL



7D



7Dtelo



Development of *Lr19/Sr25* NILs

Why – Lr19 on segment of *Agropyron elongarum* translocation to 7DL, as well as disease resistance CIMMYT breeders identified a yield advantage in some environments.

CIMMYT donors:

- Wheatear
- Kambari 1
- Oasis- no pigment

UK recurrent parents:

- Alchemy
- Paragon

Progress:

- BC2 heterozygotes selfed
- Selection with dominant marker
- WGIN COS are co-dominant so ideal for selection of homozygotes
- Third backcross made

AE Watkins and population development

Ten AE Watkins x Paragon SSD populations- now at F₄

- Extremes- height and ear emergence. Ten SSD populations up to F₅ plants in large pots, five ears bagged, 8 fully on track, the other two have winter type stragglers! [The 8 SSD pops are now sown in 1m² plots for LOLA](#)
- Thousand grain weight, grain length and grain width measured on 1100 Watkins lines. Data available on WGIN website.
- Also 2 SSDs Paragon X CS and JIC synthetic up to F₄. F₆ seed now sown and DNA extracted from F5. Already used for mapping. [SSR KASPAR integration project?](#)
- 1071 Watkins accessions in grown in soil house and at Church Farm, senescence scores taken by John Foulkes
- Watkins DNA extracted

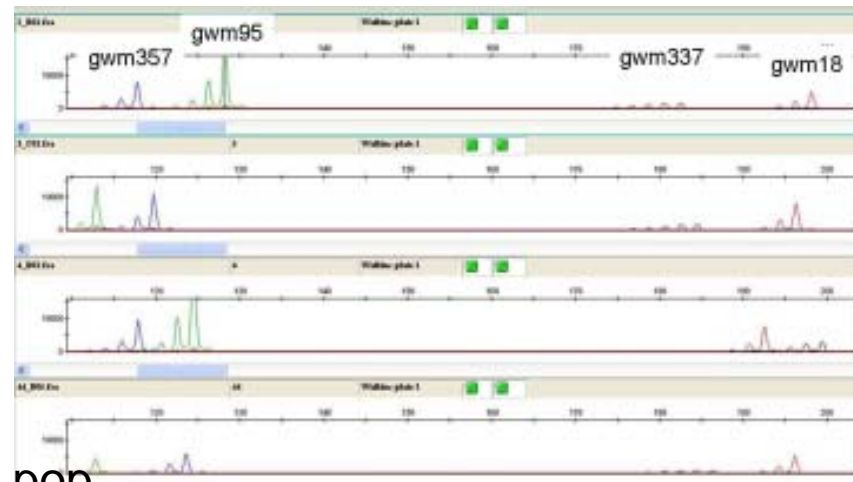


Drought population development

- 9th April meeting hosted by RAGT to discuss use of outputs from drought LINK
- Complex data set but some varieties with interesting characteristics
- WGIN will make F1s with a range of parents inc:
- Claire, Consort, Gatsby, Paragon, Timber, Zebedee, Garcia
- Further discussion to settle on strategy- **Now?**

Development of AE Watkins genotyped core sets

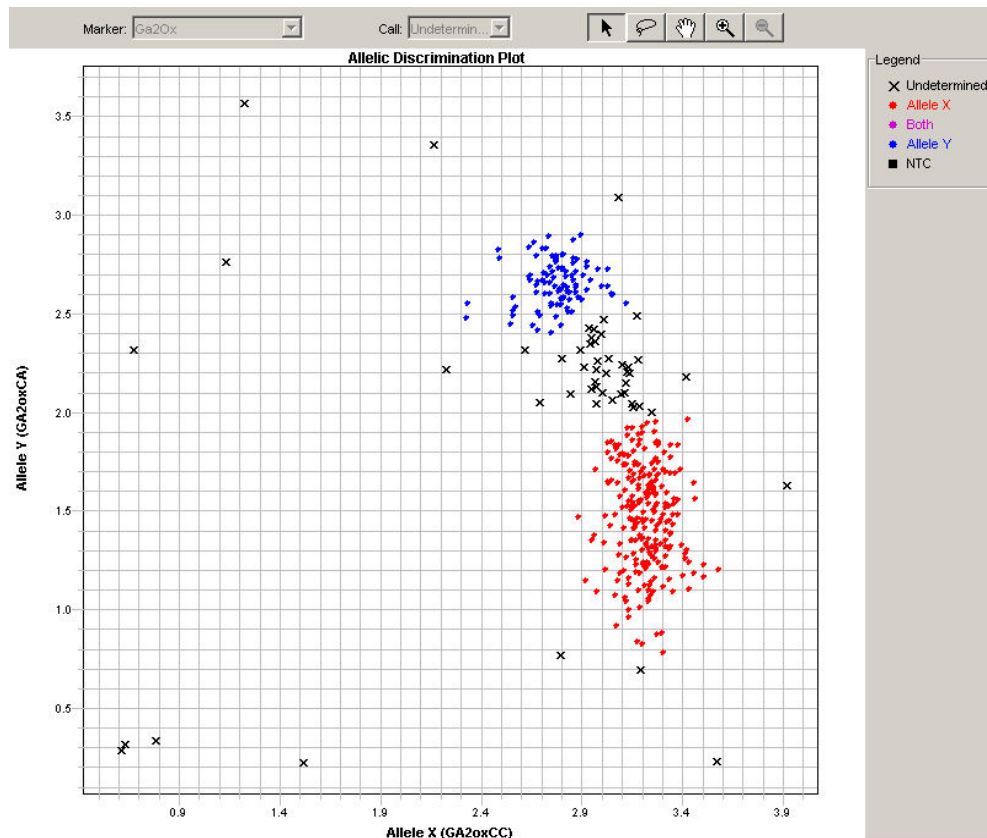
- Originally proposed DArT but more efficient to go for SSRs in anticipation of NGS profiling of relatively small (initially) core sets.



- 59 SSRs and 4 COS on full pop

- Luzie Wingen will present at WGIN stakeholders

Using AE Watkins for allele mining and association analysis



Eg GA2oxidase in collaboration
With Andy Phillips

Paragon Gamma Pops

- Over 5000 (250 Gy) irradiated Paragon
- Bringing through SSD
- Extracting DNA now for measurement of deletion rate with Bristol Uni

WGIN at JIC



Liz
Sayers



Richard
Goram

Luzie
Wingen

Simon
Orford



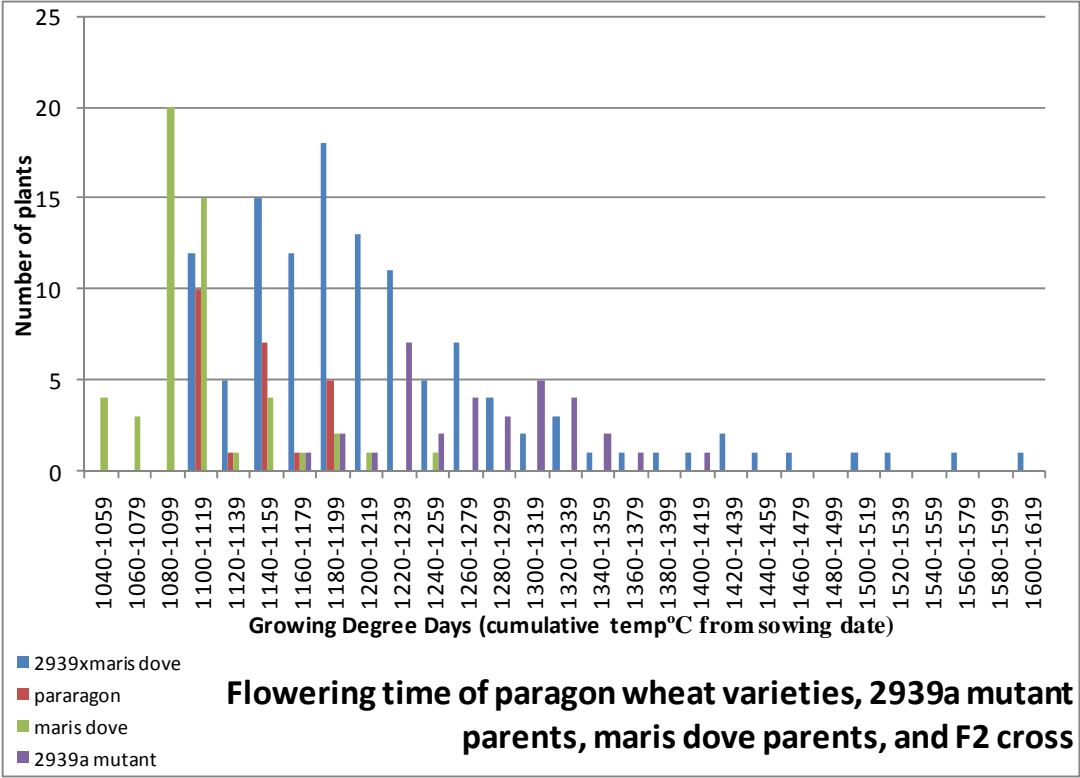
Michelle
Leverington

John
Snape

Lesley
Fish

Debora
Gasperini

Segregation of ear emergence for 2939a



Heading date DArT data returned for heading date

- 2939a mutant was crossed with Maris Dove
- 2939a mutant was crossed with Wembley
- 423a mutant was crossed with White Fife
- 423a mutant was crossed with Koga

Taking Paragon EMS alleles
forward

Tagging plants by visiting students for
DNA collection and trait scoring



Leaf senescence segregating



Mutant x Spring cultivars: F_2 families
12 families – segregations of mutant types height, flowering, leaf senescence
and biomass



Paragon mutants in Hege 80s

Left – flowering time differences (first two plots) Right – leaf senescence

'Late late' 423a






Gamma M_1 mutants:
CS bagged left (2500 sown). Paragon (2000 sown) currently bagging right
50% fertility rate expected

Now harvested M_2 seed- for sowing in spring 2010
Scope for a further 4000

Koga 7A nullisomics



Gamma mutagenesis



Objective 8 - NUE and NUE linked QTLs:
2010 trials update and plans for 2011

M J Hawkesford

WGIN management Meeting

4th November 2010

An aerial photograph of a wheat field. The field is divided into several long, parallel rows of golden-brown wheat plants. A dirt path or road runs through the field, separating the rows. The overall scene is a typical agricultural landscape.

outline

- Objectives
- Progress to date with trials etc
- 2010 data update
- Trials for 2011
- Overview of some associated work

Objectives (from application)

1. Dissect components of yield and NUE parameters in varieties of interest as identified in the preliminary screening in WGIN 1.
2. Examine physiology/biochemical processes contributing to NUE and quantify expression of key genes in selected varieties.
3. Examine variation in NUE in more 'exotic' germplasm arising from WGIN.
4. Use mapping populations to identify robust key QTLs for NUE.
5. Examine variation in early seedling nitrogen uptake ability.
6. Determine whether functionality can be maintained at reduced grain protein. This will utilise bread making quality QTLs which are independent of protein content (and known storage proteins) as identified in a previous LINK project and derived from the Hereward x Malacca population.

Workplan

- Diversity/N trials 2009-2013 (5years)
 - Core 15
 - Exotics e.g. Watkins
 - Specific A x C lines
 - Other germplasm as deemed appropriate, e.g. stay green
- Avalon x Cadenza field trials 2009/10/11 (3 years)
 - high/low N (one low, 2 high N)
 - to supplement WGIN1 trials (one high, 2 low)
- Avalon x Cadenza – G/H trial 2012
- Hereward x Malacca NILS
 - fields trials 2012/13
 - 20 lines



Diversity trial

- Germplasm
 - Core set
 - New varieties:
 - 2010: Marksman, Gallant, Oakley (Chablis)
 - 2011: Stigg, Crusoe
 - Inclusion (6 varieties) as part of BBSRC-IPA on quality-yield relationships
 - Other materials, e.g. A x C, Watkins, suggestions???
- Traits
 - Basic (WGIN-funded)
 - Yield
 - NUE etc
 - Supplementary (other funding)
 - Partitioning information
 - Analysis of post anthesis canopy longevity
 - Analysis of genotypic variation in early N-uptake efficiency

Variety Performance at 200 kg-N/ha (2004-08)

Variety	Code	Nabim	Years	Yield	%N	Uptake	Utilisation
Avalon	AV	1	5				
Flanders	FL	1	1				
Hereward	HE	1	5				
Hurley	HU	1	5				
Malacca	MA	1	5				
Mercia	ME	1	4				
Maris Widgeon	MW	1	5				
Shamrock	SH	1	4				
Solstice	SL	1	5				
Spark	SP	1	1				
Xi 19	XI	1	5				
Cadenza	CA	2	5				
Cordiale	CO	2	3				
Einstein	EI	2	1				
Lynx	LY	2	5				
Rialto	RL	2	1				
Scorpion	SC	2	1				
Soissons	SS	2	5				
Beaver	BE	3	4				
Claire	CL	3	4				
Riband	RI	3	5				
Robigus	RO	3	4				
Istabraq	IS	4	4				
Napier	NA	4	3				
Savannah	SA	4	4				
Paragon (spring)	PA	1	5				
Chablis (spring)	CH	2	1				
Arche	AR	F	1				
Batis	BA	G	5				
Caphorn	CP	F	1				
Gappelle Desprez	CD	F	1				
Enorm	EN	G	1				
Isengrain	IG	F	1				
Monopol	MO	G	5				
Opus	OP	G	1				
PBis	PB	G	1				
Petrus	PE	G	1				
Sokrates	SK	G	5				
Zyta	ZY	P	1				

Upper-Q
Inter-Q
Inter-Q
Lower-Q



Summary of variety performance (quartile rankings) based on 2004-07 WGIN datasets

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journal homepage: www.elsevier.com/locate/eja

Nitrogen efficiency of wheat: Genotypic and environmental variation and prospects for improvement

Peter B. Barraclough^{a,*}, Jonathan R. Howarth^a, Janina Jones^a, Rafael Lopez-Bellido^b, Saroj Parmar^a, Caroline E. Shepherd^a, Malcolm J. Hawkesford^a

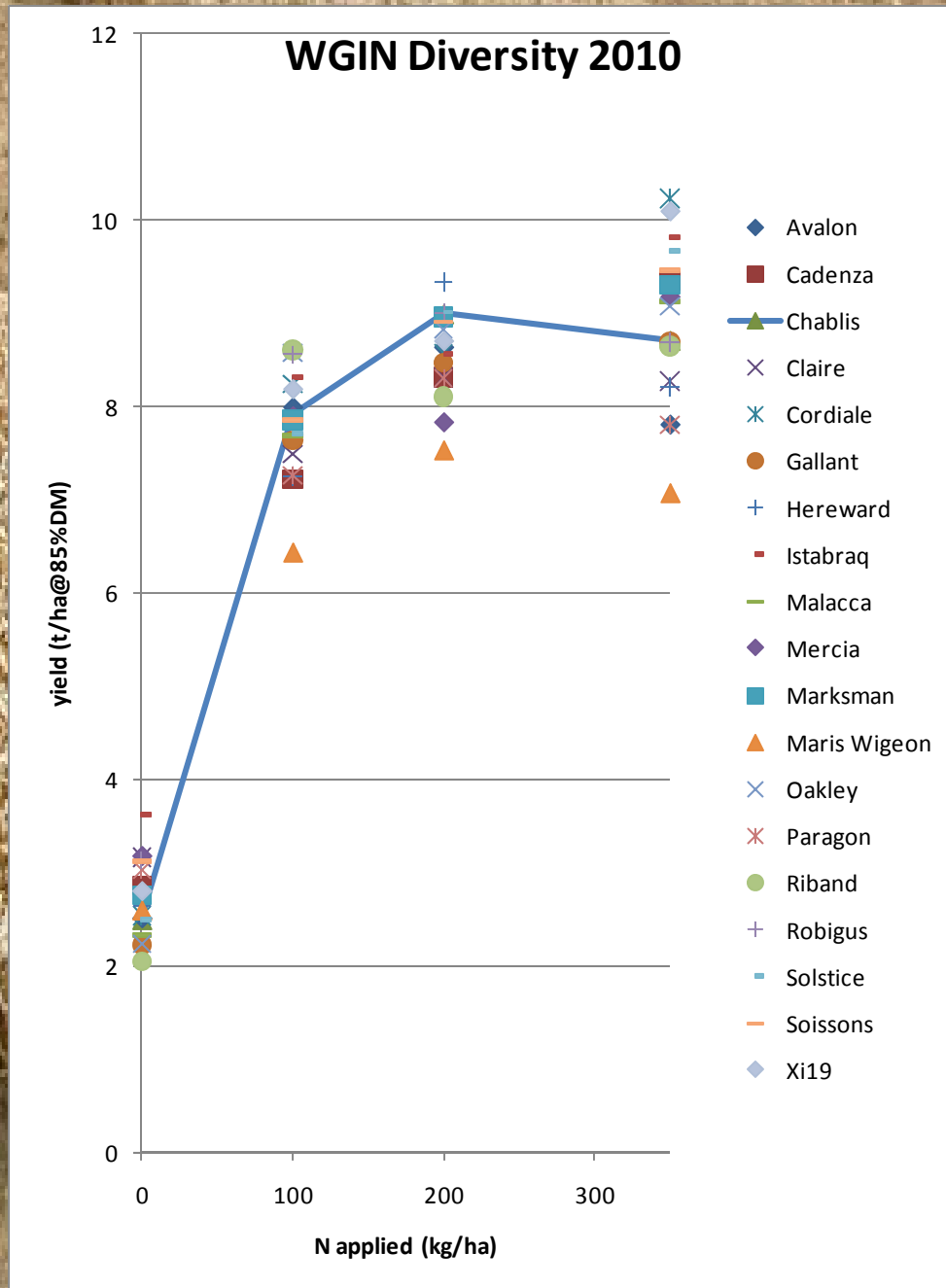
EJA (2010) 33, 1-11

Wheat varieties for WGIN-NUE 2009/10

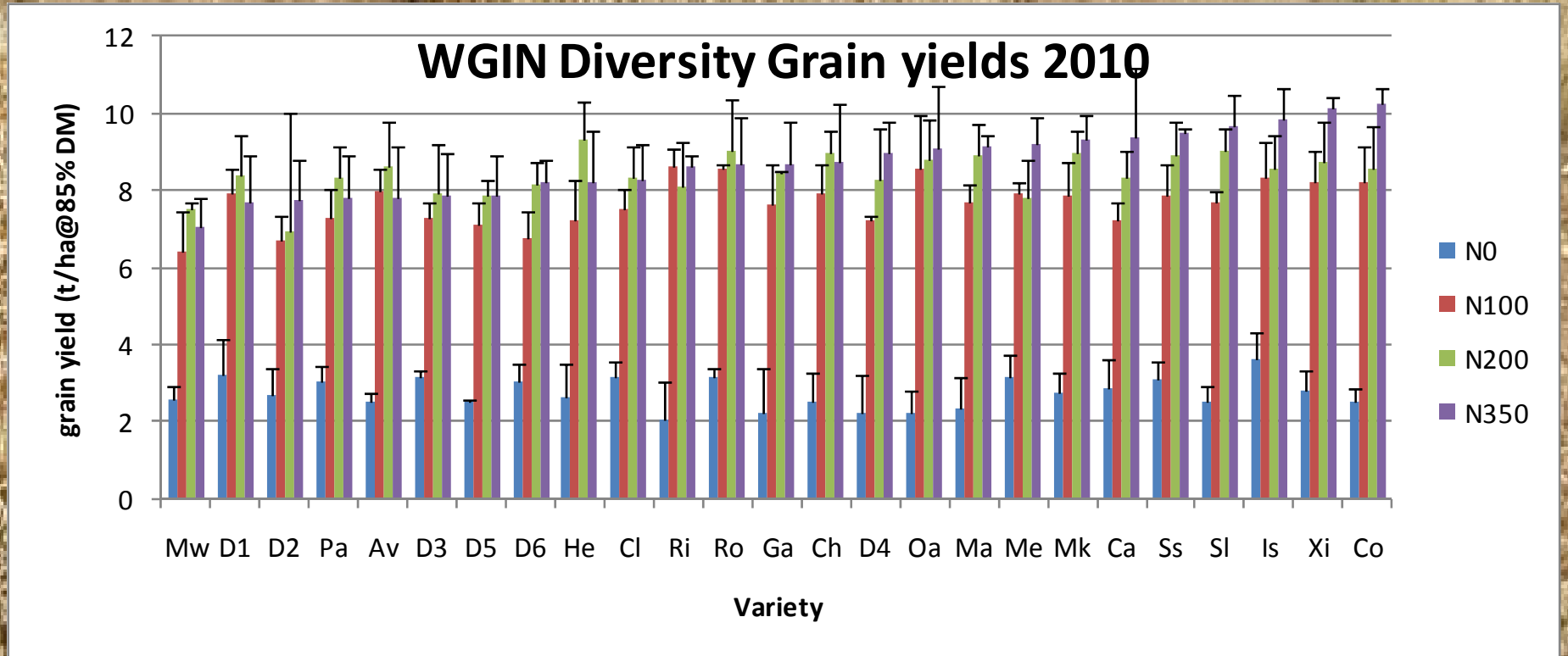
W=WGIN data, D=desk study

Variety	Code	Nabim	Rationale	inclusion in trial requested by	previous years of trials
1. Avalon	AV	1	WGIN DH parent; Low NupE & NutE (D)	PB, RG, MJH	No/05/06/07/08/09
2. Cadenza	CA	2	WGIN DH parent; Best NupE (W)	PB, RG, MJH	04/05/06/07/08/09
3. Chablis NEW 09/10		2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	MH	only in 04
4. Claire NEW 2005	CL	3	Biggest area on RL; WGIN DH parent; Good second wheat	PB,PS	No/05/06/07/08/09
5. Cordiale NEW 2006	CO	2	Good second wheat. BBSRC Quality project	RG	No/no/06/07/08/09
6. Gallant NEW 09/10		1	new claimed high yield and high protein type	MH	
7. Hereward	HE	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	PB,PS	04/05/06/07/08/09
8. Istabraq NEW 2005	IS	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat. BBSRC Quality project. WUE trial	PB,PS	No/05/06/07/08/09
9. Malacca	MA	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W). BBSRC Quality project	PS	04/05/06/07/08/09
10. Marksman	MK	2	new for 2009, PRS request for BBSRC Quality project	PS	only 09
11. Maris Widgeon	MW	1	Tall (rht), old cultivar	PB, AM	04/05/06/07/08/09
12. Mercia	ME	1	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array. WUE trial . RHT series	RG	04/no/06/07/08/09
13. Oakley NEW 09/10		4 (hard)	Hard milling type. Highest yielding wheat on RL.	MH	
14. Paragon	PA	1	Spring variety; WGIN mutagenesis population; High NupE (W)	PB	04/05/06/07/08/09
15. Riband	RI	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)	RG	04/05/06/07/08/09
16. Robigus NEW 2005	RO	3	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat. WUE trial	PB, AM	No/05/06/07/08/09
17. Soissons	SS	2	WGIN DH parent; Early maturing; High NupE, low NutE (W)	PB, RG, AM	04/05/06/07/08/09
18. Solstice	SL	2	Biggest Group 2 area; DH choice; Worst NupE (W)	RG	04/05/06/07/08/09
19. Xi19	XI	1	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W). BBSRC Quality project. WUE trial	PB,PS	04/05/06/07/08/09
20. AxC line 100			new in 2009 - high NUTE		09/
21. AxC line 116			new in 2009 - low NUTE	MJH	09/
22. AxC line 181			new in 2010 - rapid canopy senescence	MJH	10/
23. AxC line 112			new in 2010 - slow canopy senescence	MJH	10/
24. AxC line 127			new in 2009 - good early export from leaves	MJH	09/10/
25. AxC line 82			new in 2009 - slow early export from leaves	MJH	09/10/

2010 yield data



2010 yield data



Means & std dev.

2011 varieties list

Wheat varieties for WGIN-NUE 2010/11

W=WGIN data, D=desk study

Variety	Source	Code	Nabim	Rationale	inclusion in trial requested by	Previous years of trials (harvest year)
1. Avalon	Av	AV	1	WGIN DH parent; Low NupE & NutE (D)	PB, RG, MJH	05-10
2. Cadenza	Ca	CA	2	WGIN DH parent; Best NupE (W)	PB, RG, MJH	04-10
3. Chablis NEW 09/10	KWS		2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	MH	only in 04 and 10
4. Claire NEW 2005	Nick	CL	3	Biggest area on RL; WGIN DH parent; Good second wheat	PB,PS	05-10
5. Cordiale NEW 2006	KWS	CO	2	Good second wheat . BBSRC Quality project	RG	06-10
6. Crusoe NEW 10/11	Nick	CR	2	Carries dicoccoides. Shows the 'stay green' character		
7. Gallant NEW 09/10	Syn		1	new claimed high yield and high protein type	MH	
8. Hereward	RAGT	HE	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	PB,PS	04-10
9. Istabraq NEW 2005	Nick	IS	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat . BBSRC Quality project . WUE trial	PB,PS	05-10
10. Malacca	KWS	MA	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W). BBSRC Quality project	PS	04-10
11. Marksman	RAGT	MK	2	new for 2009, PRS request for BBSRC Quality project	PS	only 09 and 10
12. Maris Widgeon		MW	1	Tall (rht), old cultivar	PB, AM	04-10
13. Mercia		ME	1	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array. WUE trial . RHTRG series	RHTRG	04 and 06-10
14. Oakley NEW 09/10	KWS		4 (hard)	Hard milling type. Highest yielding wheat on RL.	MH	
15. Paragon	RAGT	PA	1	Spring variety; WGIN mutagenesis population; High NupE (W)	PB	04-10
16. Riband	RAGT	RI	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)	RG	04-10
17. Robigus NEW 2005	KWS	RO	3	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat . WUE trial	PB, AM	05-10
18. Stigg NEW 10/11	Nick	ST	?4	Carries dicoccoides. High disease resistance. Shows the 'stay green' character		
19. Soissons	Elsoms	SS	2	WGIN DH parent; Early maturing; High NupE, low NutE (W)	PB, RG, AM	04-10
20. Solstice	Nick	SL	2	Biggest Group 2 area; DH choice; Worst NupE (W)	RG	04-10
21. X119	Nick	XI	1	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W). BBSRC Quality project . WUE trial	PB,PS	04-10
22. AxC line 181		D3		new in 2010 - rapid canopy senescence	MJH	10/
23. AxC line 112		D4		new in 2010 - slow canopy senescence	MJH	10/
24. AxC line 127		D5		new in 2009 - good early export from leaves	MJH	09/10/
25. AxC line 82		D6		new in 2009 - slow early export from leaves	MJH	09/10/

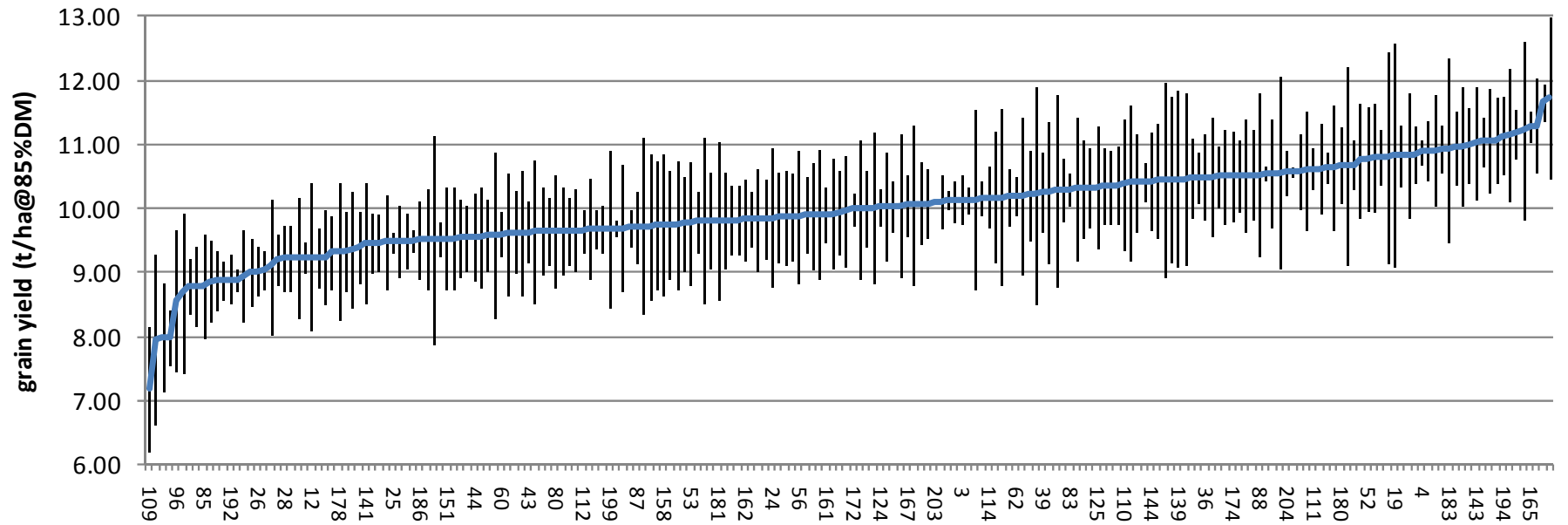
A x C traits - Rothamsted

- Core data (WGIN)
 - Flowering time and height
 - Yield (grain and straw) and tgw
 - Nitrogen (grain and straw)
 - Computed NUtE, N uptake (final)
- Supplementary studies (other)
 - Leaf N and SPAD (anthesis and 21 dpa)
 - Leaf size (leaf 2)
 - Canopy longevity, reflectance, rate of senescence
 - Early N uptake
 - Gene expression
 - Root traits
 - Grain minerals

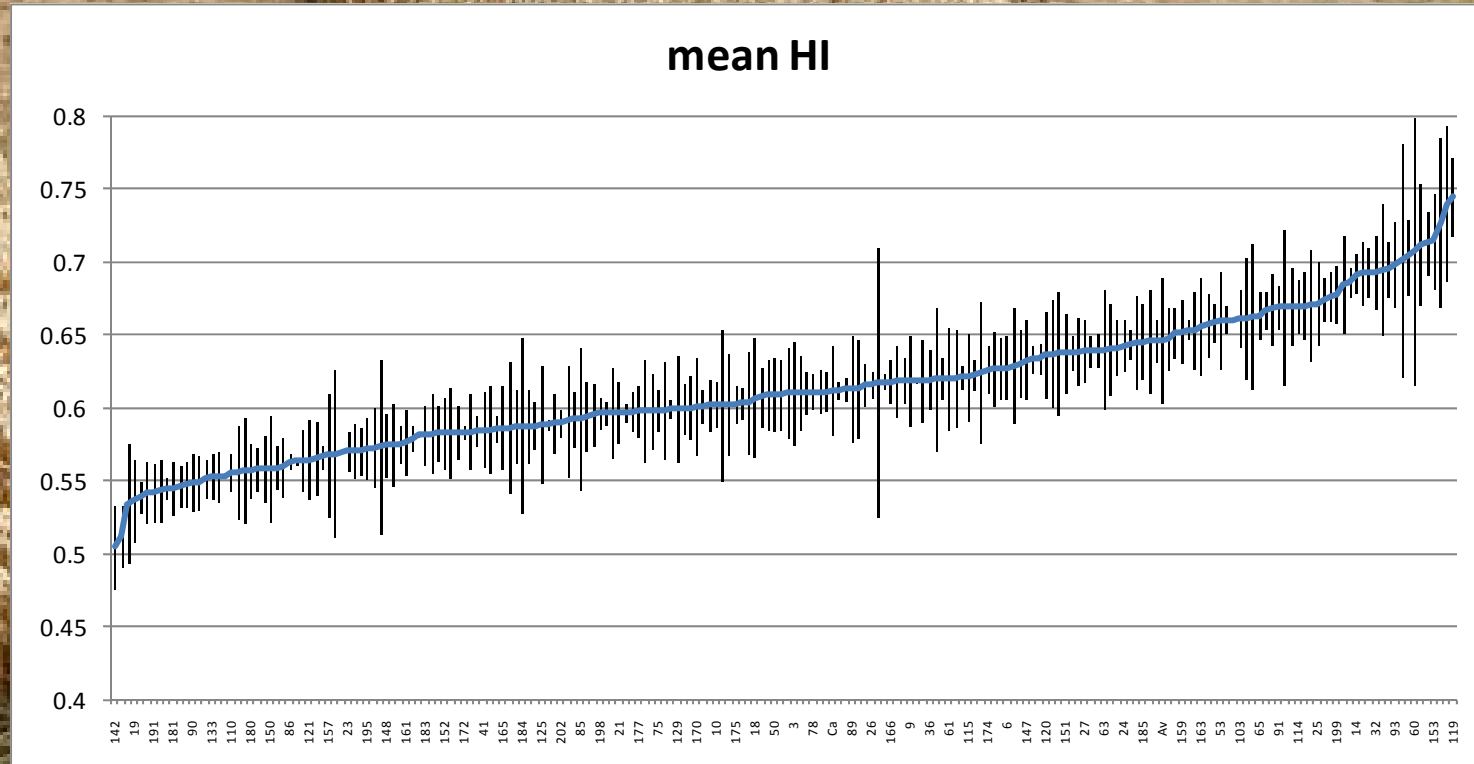


Yields 2010

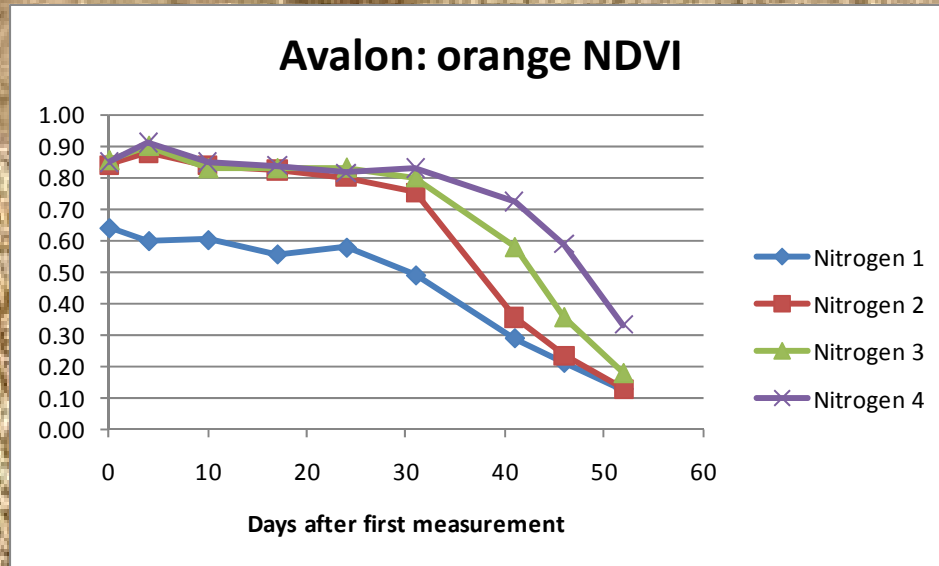
Rothamsted A x C 2010 200 kgN/ha



HI, 2010



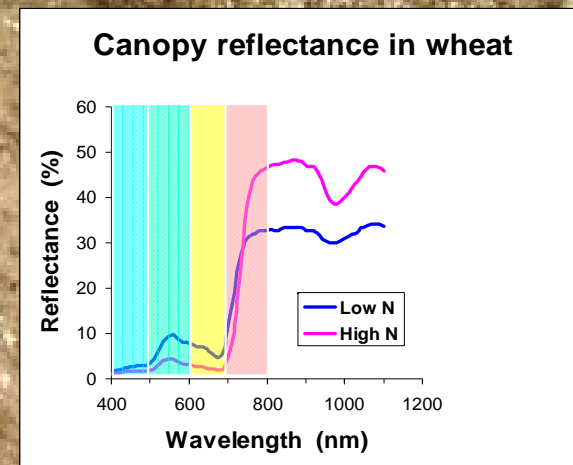
Senescence monitoring → QTLs



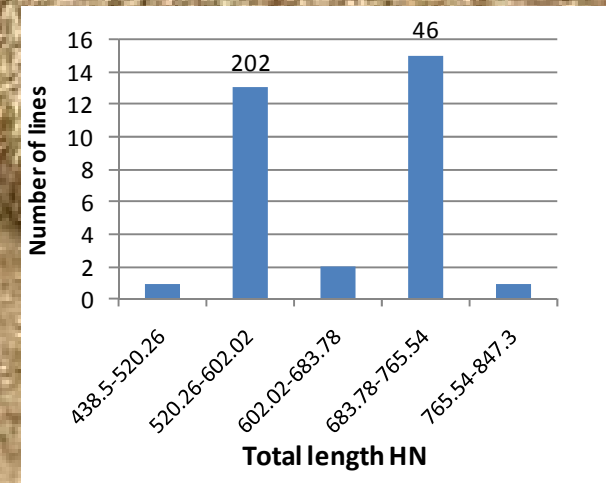
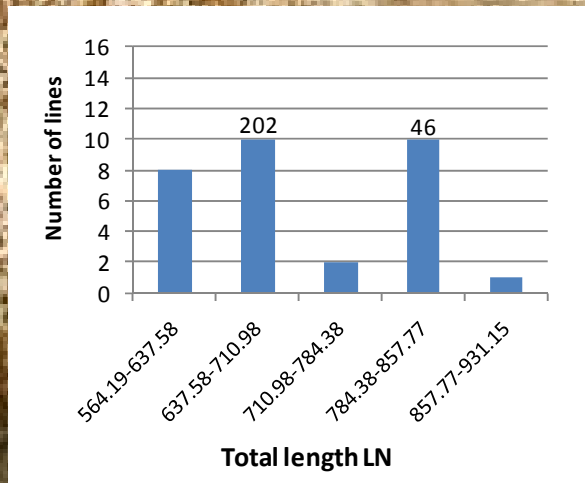
Datasets;
A x C and Diversity for both
2009 and 2010



$$o\text{NDVI} = \frac{750 - 680}{750 + 680}$$



Root traits – mapping QTLs



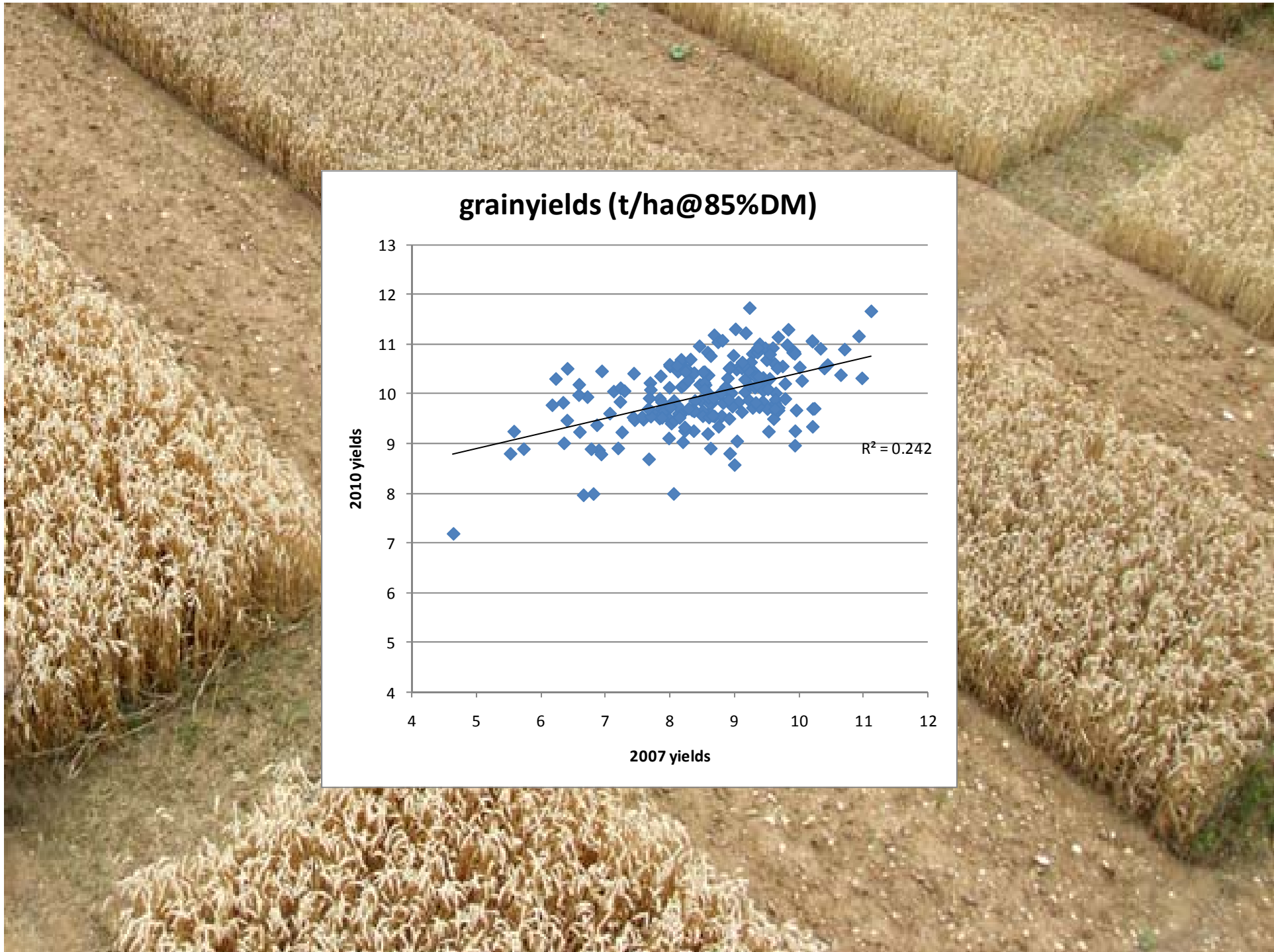
WinRHIZO 2008 (Caihong Bai)



Thanks

- Peter Barraclough
- RRes Farm staff
- Group and field team: Peter Buchner, Yongfan Wan, Jonathan Howarth, Mark Durenkamp, Saroj Parmar, Janina Jones, Dan Godfrey, Emmanuelle Cabannes, Adinda Derkx, Fumie Shinmachi, Caihong Bai + many summer students
- WGIN team

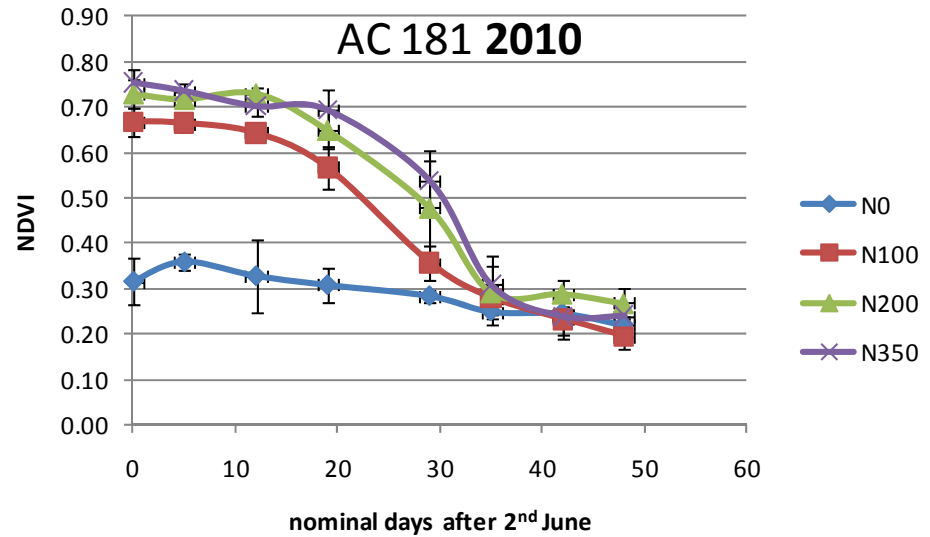




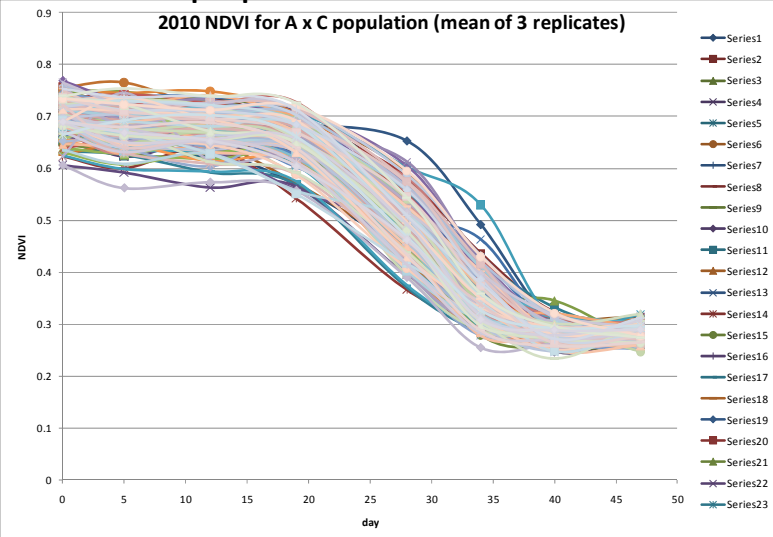


Nitrogen efficiency of wheat: Genotypic and environmental variation prospects for improvement

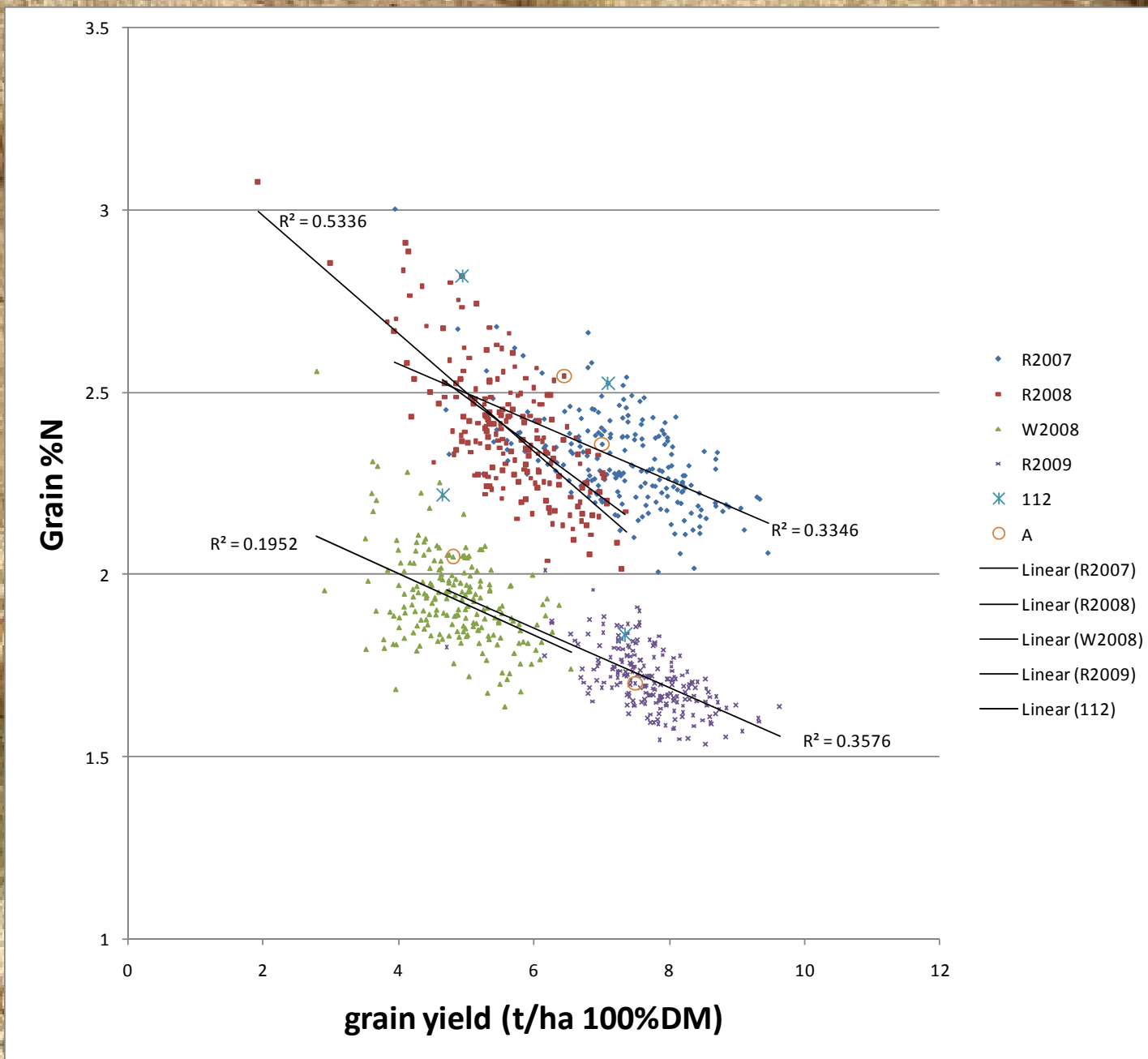
Peter B. Barraclough^{a,*}, Jonathan R. Howarth^a, Janina Jones^a, Rafael Lopez-Bellido^b, Saroj Parmar^a, Caroline E. Shepherd^a, Malcolm J. Hawkesford^a



Entire population



Yield v grain %N



Extending the A × C mapping population

November 2007 – RRes provided F₁ seeds of the 'Avalon × Cadenza' and reciprocal 'Cadenza × Avalon' crosses to Lochow-Petkus GmbH (Einbeck, Germany)



July 2008 – Lochow-Petkus returned to RRes > 1000 putative DH lines



August-September 2008

- DNA was extracted from all plants
- Plants were vernalised and grown to maturity under glass



December 2008

Recovered*:

- > 30 grains from 484 plants
- 1-10 grains from another 98 plants

* All other ~ 500 plants were probably haploids as they failed to set seed

Extending the A × C mapping population

2009-2010 Season

484 new A x C DH lines were grown in a field on the ex-fallow land
Two 75-cm rows per line / 15 grains per row



Summer 2010 - hand harvested more than 140g seed / line for most lines

Phenotypes observed during the 2009-2010 field season

Variation in height



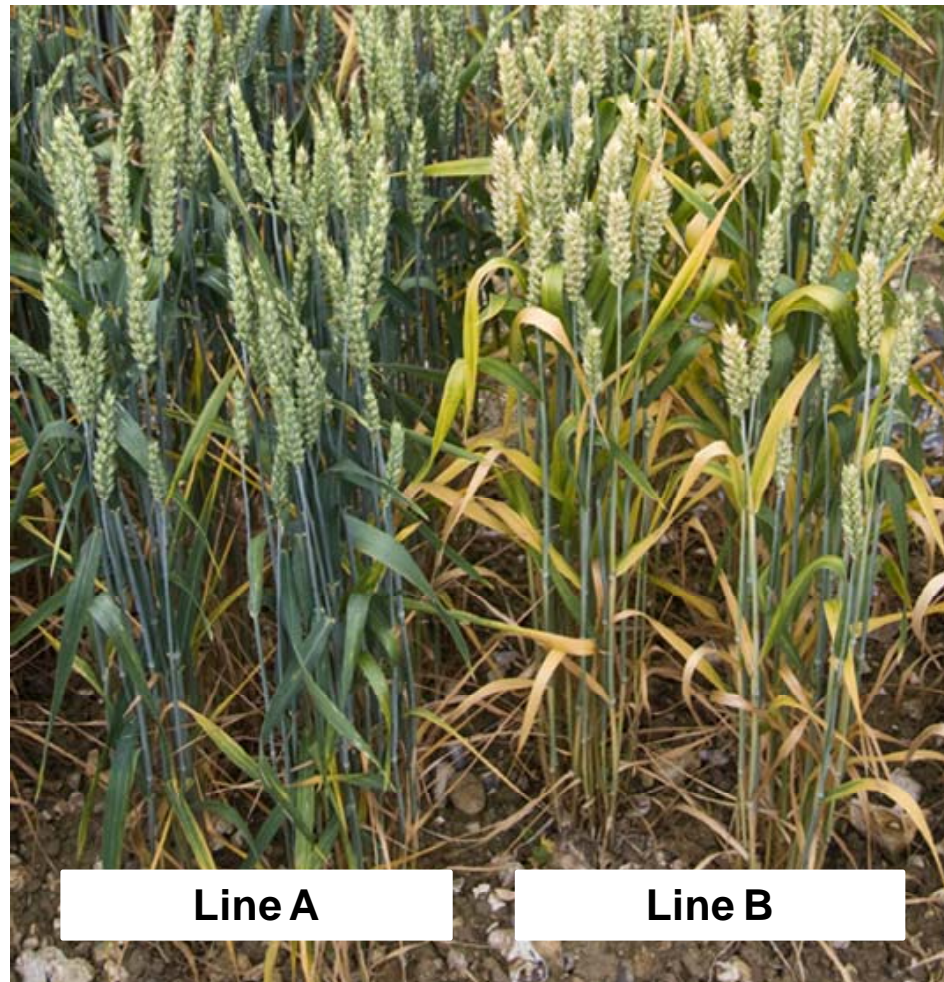
Phenotypes observed during the 2009-2010 field season

Variation in variation in ear colour (green / yellow)



Phenotypes observed during the 2009-2010 field season

Variation in senescence date



The first batch of 484 new A × C DH lines

- **Small quantities of seed** are now available upon request for small research projects.
- **DNA from these lines** will be available for use on a collaborative basis from mid November 2010.
- Twenty two lines are currently (2010-2011 season) being multiplied on 1.8-m x 3-m field plots, and **445 lines – on 1.8-m x 6-m plots.**
- Medium/large quantities of seed **from these 467 new DH lines** will be available for field experimentation **from late summer 2011. We expect to harvest ~ 4-5 kg seed per each line.**
- The remaining **17 new DH** lines are currently being multiplied on small plots comprising of three 50-cm rows per line (20 seed per row). These lines will be available for projects involving small plots from late summer 2011, and for those involving large plots – from late summer 2012.

Extending the A×C mapping population

December 2008

1-10 grains from another 98 plants received from Lochow-Petkus

2009-2010 Season

98 new DH lines were grown in a glasshouse (1-5 plants per 21-cm pot)



In Spring 2010 - hand harvested 100 - 3,000 grains / line for most lines

The second batch of 98 new A×C DH lines

- **DNA from these lines** is already available for use on a collaborative basis
- All 98 DH lines are currently (2010-2011 season) being multiplied in the field on small plots comprising of three 50-cm rows per line (20 seed per row)
- Small quantities of seed from these lines will be available upon request for small research projects from late summer 2011
- Medium/large quantities of seed will be available for field experimentation from late summer 2012

New look A×C mapping population

- **205** 'original' lines (JIC) – lots of seed
- **467** new lines (Rothamsted) – seed for small pot experiments is already available; larger seed quantities will be available for field trials from late summer 2011
- **115 (98 + 17)** additional new lines (Rothamsted) – seed for small pot experiments and for field trials will be available from late summer 2011 and late summer 2012, respectively

Total = **787**

The A x C cross was originally selected by Steve Parker (CSL), late Tony Worland (JIC) and Darren Lovell (LARS-RRes) for studies of canopy architecture traits in collaboration with ADAS and the University of Nottingham



Many thanks to



Ian Crute

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Clemens Springmann

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Joseph Whittaker (BBSRC)

Marcin Czaban (WGIN)

James Bruce (HGCA-BBSRC)

Resistance to Take-all

Richard Gutteridge
Kim Hammond-Kosack



WGIN MM@RRes
4th Nov 2010

Take-all disease of wheat

- *Gaeumannomyces graminis*
var. *tritici* (**Ggt**)
 - ascomycete soil borne fungus
 - related to rice blast fungus
Magnaporthe oryzae (previously
M. grisea)



Severely infected take-all plant

A *Ggt* infected wheat root

Take-all
lesion

Runner hypha



Take-all disease – soil-borne fungus

In 1st wheats - no disease problem



A major problem
for 2nd / 3rd wheat crops

2nd wheat syndrome

The risk of take-all is largely dependent on the amount of fungal inoculum in the soil at the time of sowing



Typical take-all patch showing stunting
and premature ripening of the crop

Objective 10 - Talk Outline

- **Hexaploid wheat – Watkins / Gediflux collections
Diploid wheat + Tetraploid wheat**
 - field evaluation to identify potentially resistance genotypes
- **Diploid wheat**
 - mapping populations
- **Hexaploid wheat – inoculum build-up in 1st wheats**
 - results so far / current activities

Watkins Hexaploid wheat collection

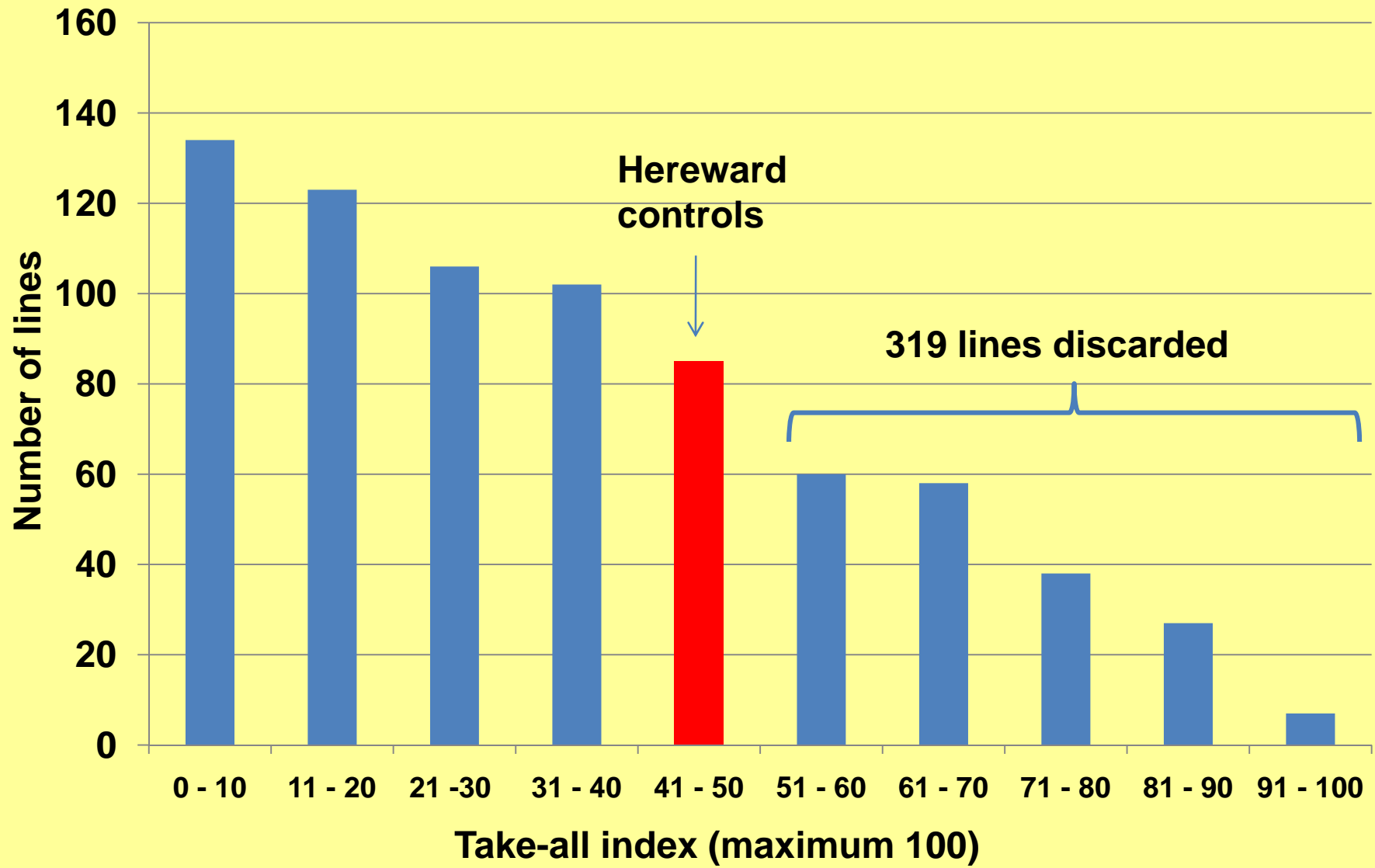
Take-all / eyespot assessments

- **2008 and 2009 field season – one plot / genotype – established from 45 seeds**
- **823 lines from the collection (both years – 740 lines)**

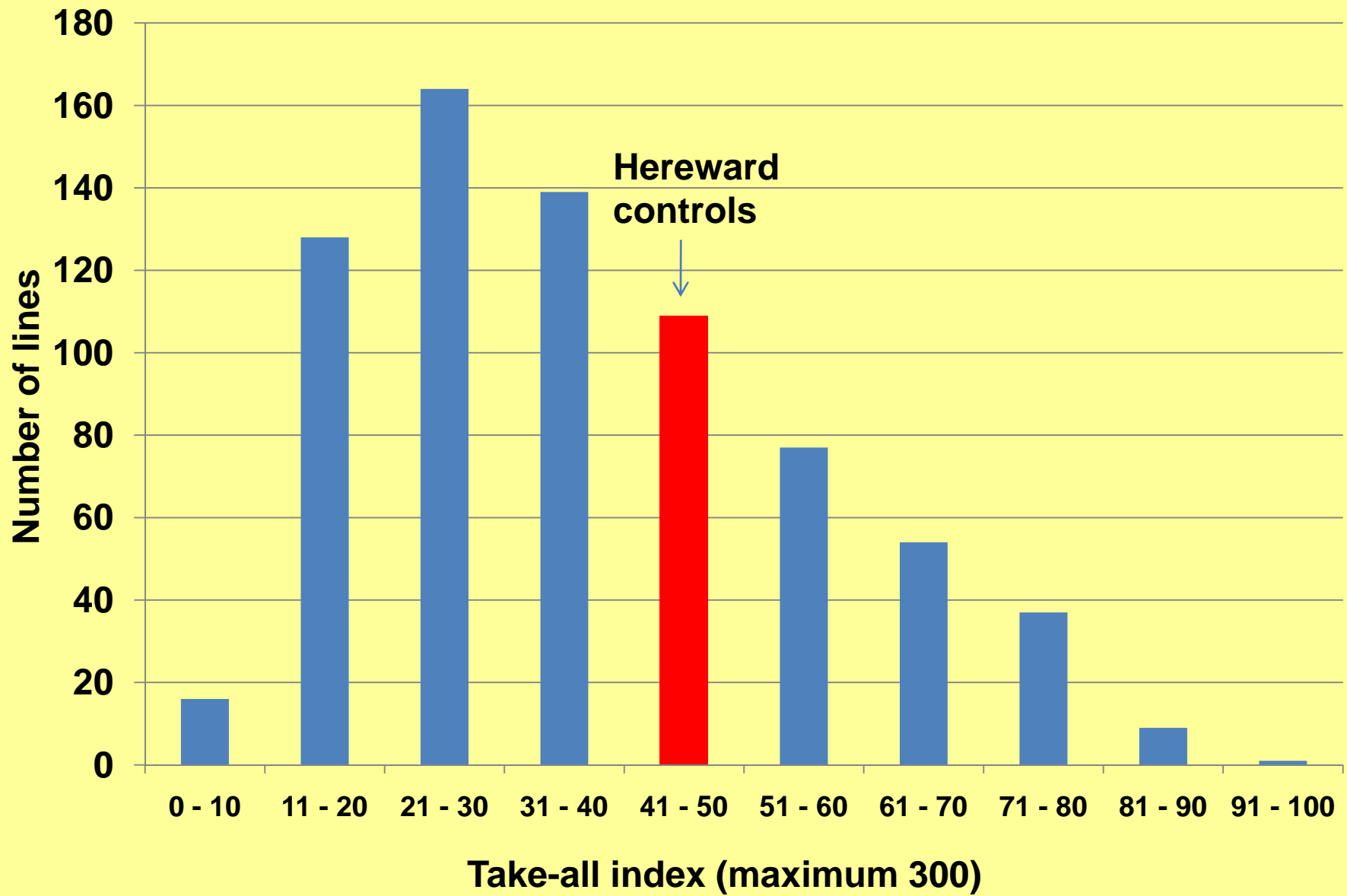


3rd wheat situation

Watkins 2008 Take-all data



Watkins 2009 Take-all data



Watkins/Gediflux Hexaploid wheat collection

Aim: To identify genotypes with tissue based resistance

Watkins lines

823 lines tested of which **319** discarded as take-all susceptible (2008 season).
2009 season still in statistical analysis – next intercompare the 2 years of data

Gediflux collection – 24 lines from 60 lines originally tested have been discarded from the 2009 assessments.

2010 – 2011 field season (year 3)

504 Watkins lines and **36 Gediflux lines**

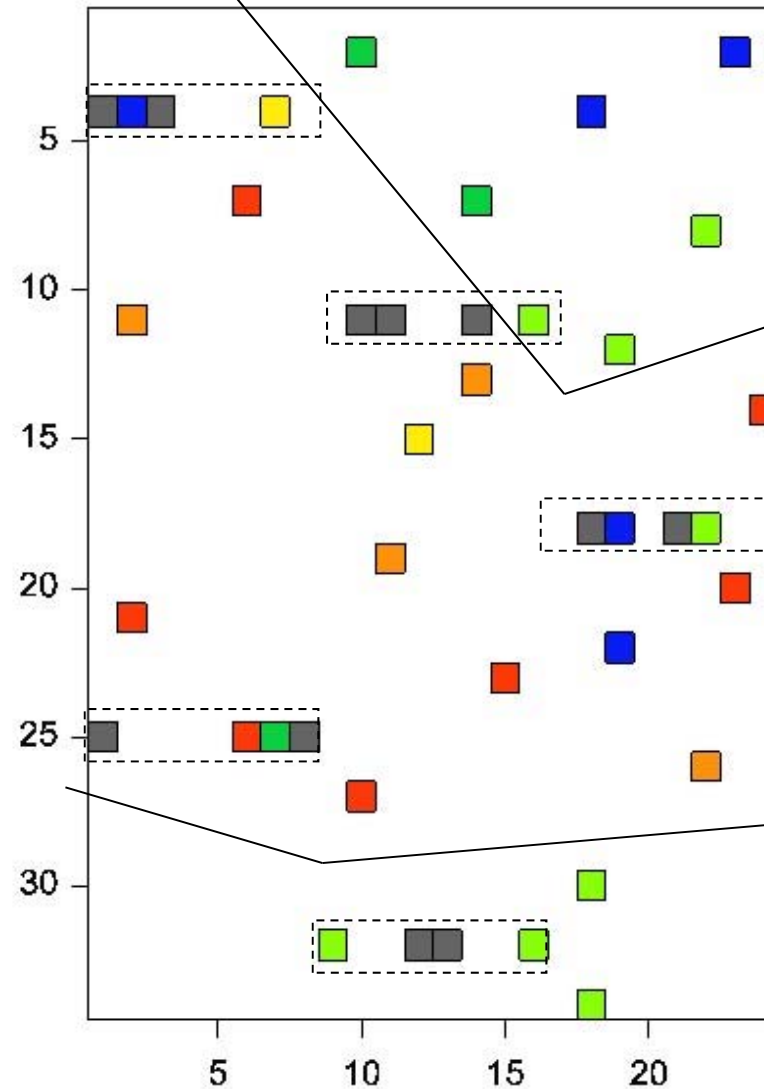
5 blocks of 8 controls

20 Hereward control plots.

Sown 21st October 2010 – Claycroft field 3rd wheat

Watkins Experiment 2008 RRes Take-all severity - control plots

Takeall index



Alpha design

N = 800 plots

5 control blocks

Variety	TAI
Hereward	35.6
Triticale	18.4
Rye	1.7
Oats	0.0

TAI

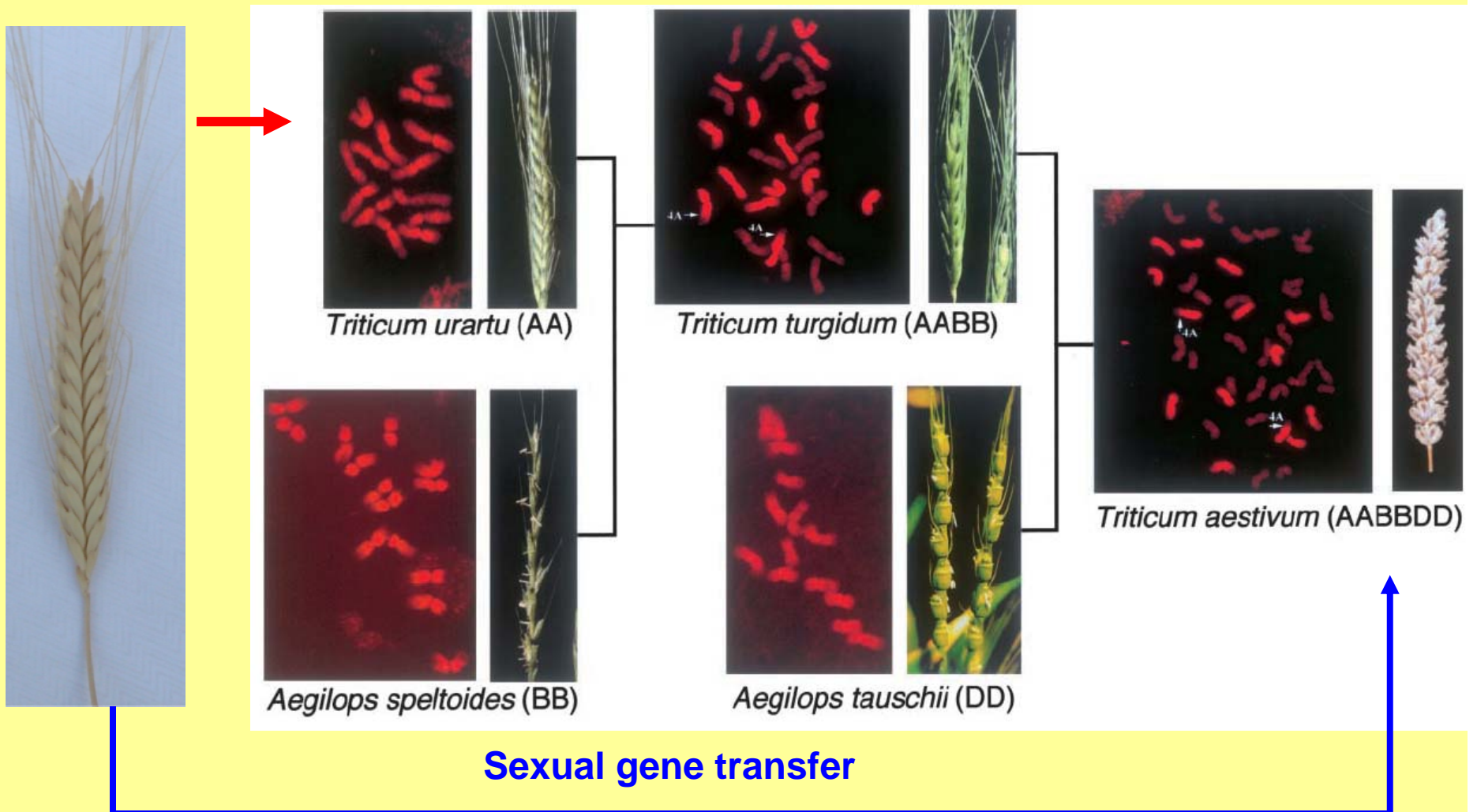
0-5
6-15
16-25
26-35
36-45
46-55
> 55

Mean of all plots
Hereward = 43.4

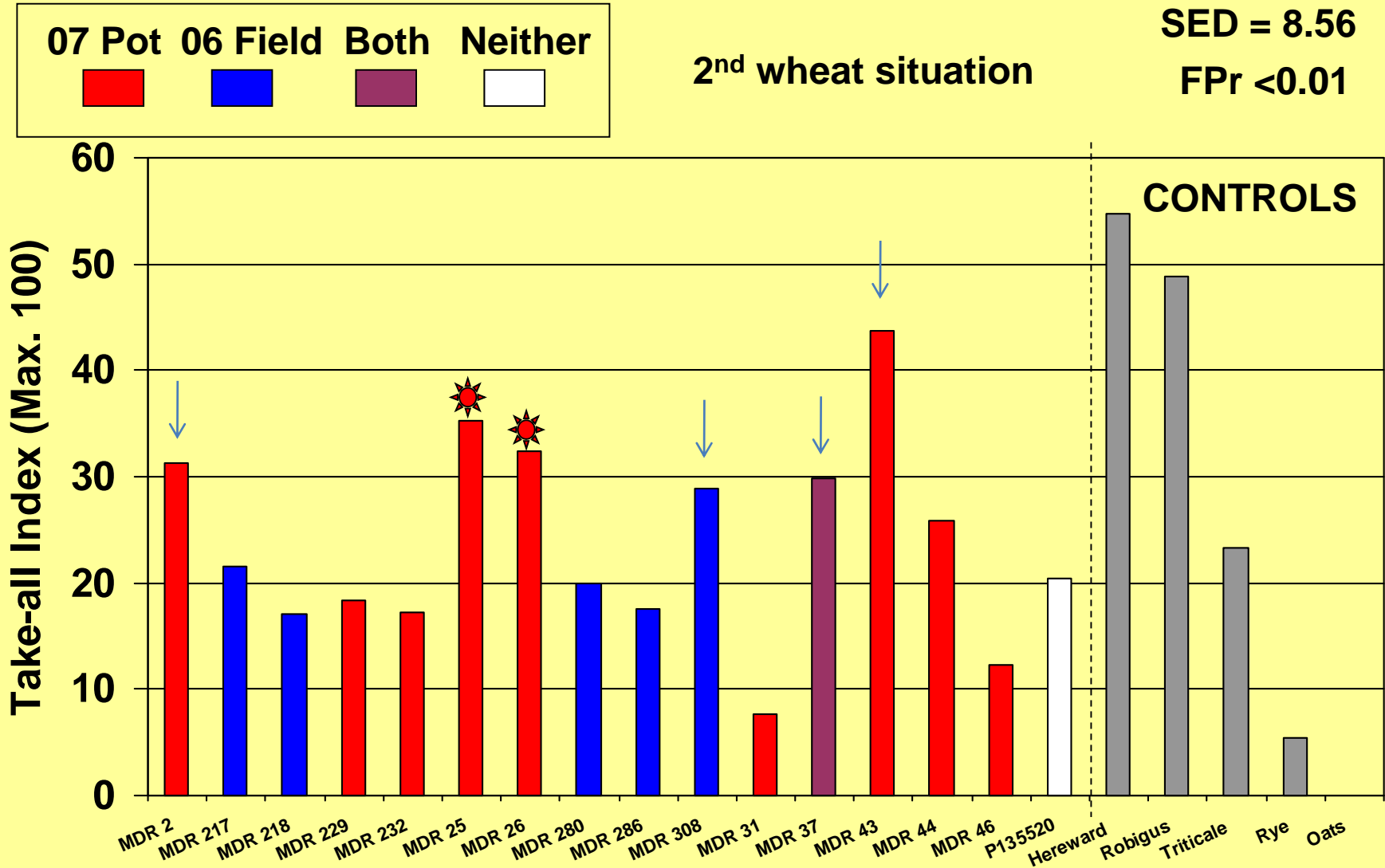
Hereward - Extra 20 plots - mean TAI = 45.3

Origin of bread wheat

T. monococcum A^mA^m

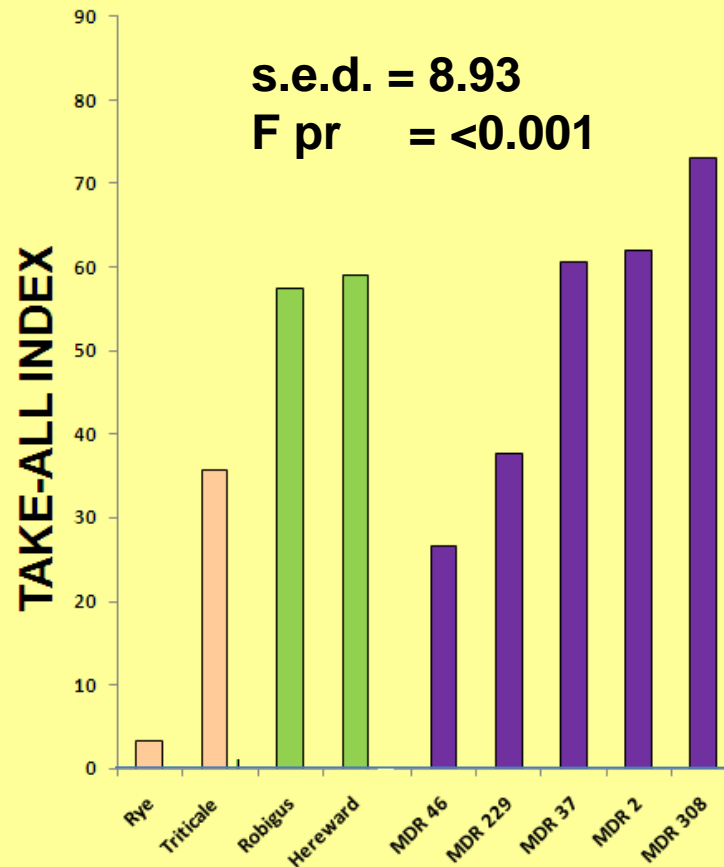


Field experiment 2008



5 rep exp but 10 reps MDR 37, MDR 46 and MDR 229

Diploid *T. monococcum* - Field experiment 2009



MDR 308 is DV92 (Dubcovsky)

Diploid Field experiments 2009 - 2011

2009	2010		2011	
37	31	280	31	280
229	46	286	46	286
2	217	P135520	217	P135520
308	218	2	218	2
46	229	308	229	308
	232	37	232	37

2010 experiment sampled, processed and in store. Awaiting assessment.

Sown 22nd October 2010 - Claycroft field 3rd wheat

T. monococcum - Glasshouse crosses

2008

MDR037 x MDR046 →
MDR037 x MDR229 →

2009

F₂

2010

F₃

~ 120 lines
SSD for
each popⁿ
(resown)

2011

Harvest F₄
Feb
onwards

↓
Take-all pot test
(~30 seed / line)

2009

	Male	MDR043	MDR024	MDR037	MDR308	MDR002	MDR031	MDR046	MDR229	MDR217	MDR650
Female		S	S	S	S	S	R	R	mR	mR	mR
MDR043	S	■	28	0	15	11	28	6	11	59	18
MDR024	S	10	■	X	X	X	40	15	2	13	X
MDR037	S	X	X	■	X	X	28	26	5	31	X
MDR308	S	X	X	X	■	X	43	23	60	62	48
MDR002	S	X	X	X	X	■	48	36	31	32	13
MDR031	R	9	28	4	6	13	■	20	2	38	X
MDR046	R	4	11	2	2	X	10	■	X	30	X
MDR229	mR	16	50	0	X	X	9	X	■	X	X
MDR217	mR	14	X	X	X	X	4	X	X	■	X
MDR650	mR	40	X	X	X	X	X	X	X	X	■

■ < 10 grain X = not done

2010

Completing some
additional reciprocal crosses

Sown many of the F₁s

Main focus

R / mR – MDR031, MDR046, MDR 229

S – MDR037, MDR 043, MDR308

Talk Outline

- Hexaploid wheat – Watkins / Gediflux collections
Diploid wheat + Tetraploid wheat
 - field evaluation to identify potentially resistance genotypes
- Diploid wheat
 - mapping populations
- Hexaploid wheat – inoculum build-up in 1st wheats
 - results so far / current activities

Take-all and inoculum build up WGIN 1

Background

- The risk of take-all is largely dependent on the amount of inoculum in the soil at the time of sowing
- **A soil core bioassay, taken after harvest**, is used to measure the take-all infectivity of the soil
- Results from WGIN 1 have suggested that varieties can build up the take-all fungus differentially when grown as a first wheat.

Take-all infectivity of the soil after different winter wheat cultivars - WGIN bioassay

The bioassay data from 2004 – 2008 is now on the website

V. E. McMillan, K. E. Hammond-Kosack and R. J. Gutteridge (2010)

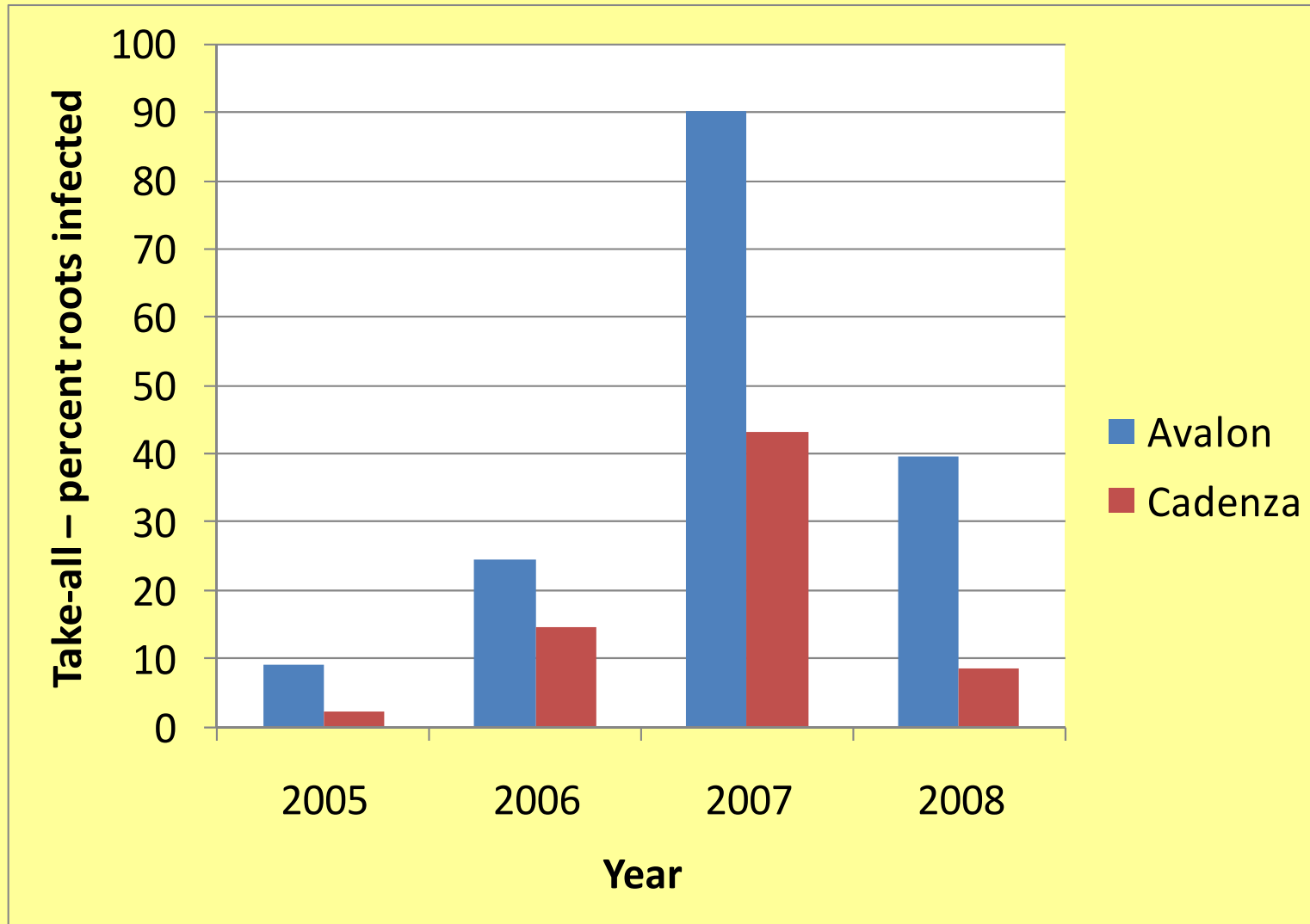
Evidence that wheat cultivars differ in their ability to build-up inoculum of the take-all fungus, *Gaeumannomyces graminis* var. *tritici*, under a first wheat crop

Available early on line in Plant Pathology
+ copy on WGIN website

Cadenza - low Take-all Build up - LowTAB cultivar

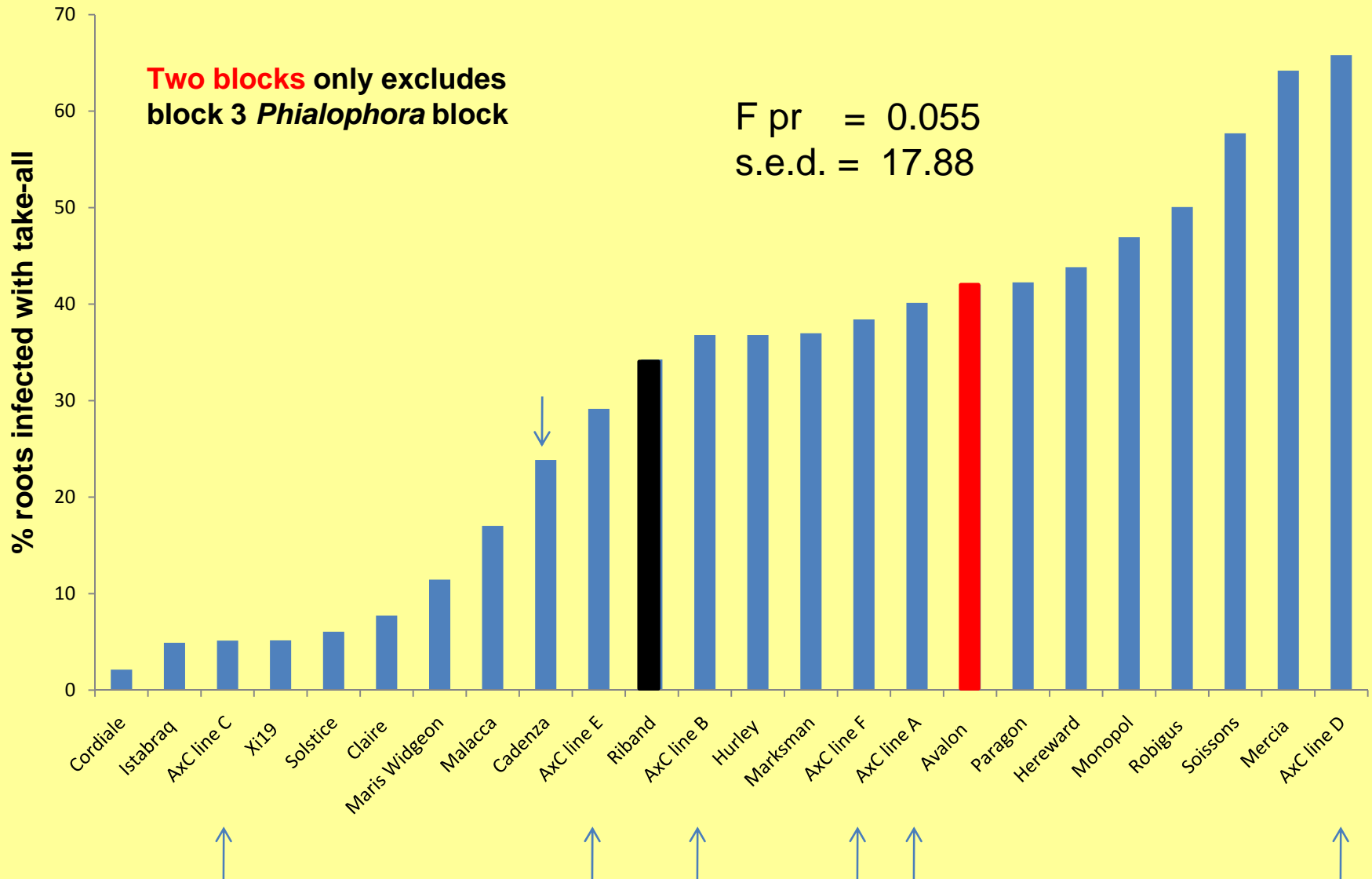
Avalon - high Take-all Build up - HighTAB cultivar

% roots infected with take-all in a soil core bioassay Avalon and Cadenza 2005 - 2008 WGIN Diversity trials



WGIN winter wheat bioassay 2009

Take-all infectivity in the soil after different winter wheat varieties
WGIN Diversity NUE trial – at harvest



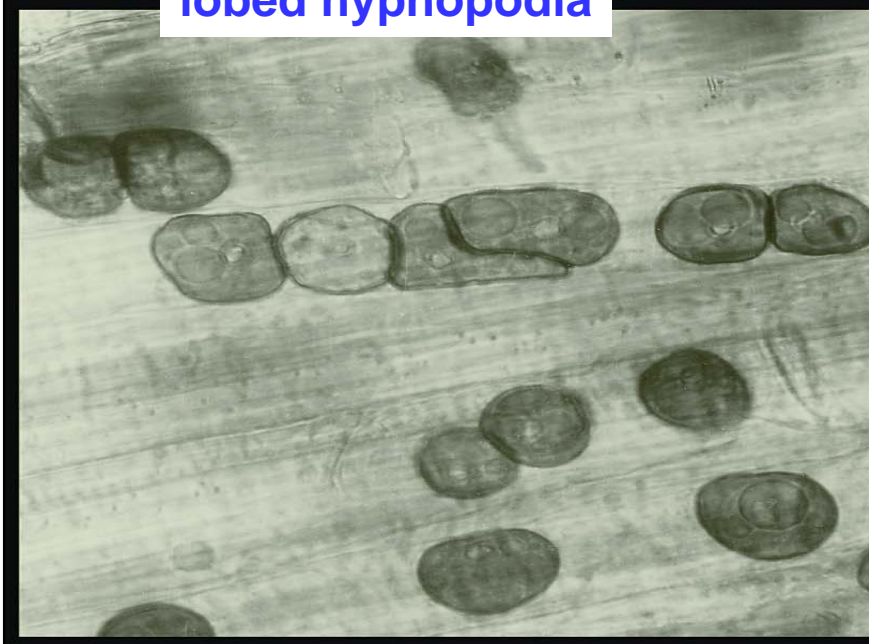
Symptoms of *Phialophora* on wheat roots



Phialophora spp.
lobed hyphopodia



Phialophora graminicola



Avalon x Cadenza mapping population bioassay – Some stats !!!

Experiment **208 plots x 3 replicates** = 624 plots
5 sample sites per plot each into a single cup

Time for preparation, sampling and set-up bioassay:

Drilling holes for cups pre-filling (3120) = 10 hrs

Label cups & re-organise in plot order = 45 hrs

Soil core sampling = 100 hrs

936 Kg of soil removed from the field

Re-organise to pot order = 20 hrs

Sow and transfer to CE room = 120 hrs

Wash and prepare for take-all assessment = 100 hrs

Take-all assessment = many hours



Many thanks to



RRes Farm staff

Richard Gutteridge

Vanessa McMillan (HGCA-BBSRC)

Kostya Kanyuka

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Steve Freeman (WGIN casual)

Elke Anzinger

Summer students

Nicola Phillips (HGCA)

Joseph Whittaker (BBSRC)

Marcin Czaban (WGIN)

James Bruce (HGCA-BBSRC)